

REMARKS

Applicants have studied the Office Action of November 29, 2000 ("Office Action"), and have made amendments to the claims. It is respectfully submitted that the application, as amended, is in condition for allowance. Claims 1-71 are pending in the present application. In previous amendments, the Applicant withdrew claims 12-18 and 20-23 from consideration, canceled claims 3 and 4, and added claims 24-42. In the present Preliminary Amendment, the Applicant has cancelled claims 1-2, 5-9, 11, 19 and 24-42 and added claims 43-71. No new matter has been added. Reconsideration and allowance of the claims in view of the above amendments and the ensuing remarks are respectfully requested.

The Examiner objected to independent claims 1, 5, and 8 and the claims that depended from them under 35 U.S.C. 112, first paragraph, stating that the specification does not enable one to isolate a nucleic acid sequence that has at least 60% homology to the nucleotide sequence of SEQ ID NO:2 or SEQ ID NO:3. The Examiner stated that "no guidance is provided as to which of the myraid of nucleic acid sequences encoding polypeptide sequences encompassed by the claim will retain the characteristics of a TfR2."

The Applicant has canceled claims 1, 5, and 8 and replaced them with new independent claims 43 and 63 that do not recite the limitation "having at least 60% homology."

Independent claim 43 is directed to an isolated nucleic acid molecule comprising a nucleic acid encoding a polypeptide having a sequence defined by the amino acid and nucleotide sequences recited in the specification, namely, SEQ ID NO:1, SEQ ID NO:2, and SEQ ID NO:3. Claim 43 does not recite nucleic acid sequences "having at least 60% homology" to the sequences of SEQ ID NO: 2 or 3. The Applicant respectfully submits that claim 43 fully comports with the requirements of 35 U.S.C. § 112, first paragraph.

Independent claim 63 is directed to an isolated nucleic acid sequence comprising a nucleic acid that is substantially the same as the nucleic acid sequences of SEQ ID NOS: 2 or 3. The degree of homology of this isolated nucleic acid sequence to the nucleic acid sequence of SEQ ID NOS: 2 and 3 is defined by a functional test recited at page 28 of the specification ("Tf-binding to the TfR2- α Transfected Cells"). Under this

test, one transfects a cell that lacks transferrin receptors, such as a CHO-TRVb cell, with the nucleic acid whose function is desired to be tested (for example, the TfR2- α sequence as defined by SEQ ID NO: 2). One then incubates the cells with transferrin and determines if the cells bound it. Claim 63 recites this test with specificity: "the nucleotide is transfected into a cell that lacks transferrin receptors and the cell is incubated with 5 μ g/ml of transferrin in nutrient media for 30 min on ice." Claim 63 requires that the nucleotide sequence it recites "encodes a polypeptide that binds transferrin" when tested in this manner.

The Applicant respectfully submits that claim 63 fully comports with the requirements of 35 U.S.C. § 112, first paragraph. The Examiner found claims 1 and 8 "overly broad in their recitation of '60% identical' since no guidance is provided as to which of the myriad of nucleic acid sequences encoding polypeptide sequence encompassed by the claim will retain the characteristics of a TfR2." New claim 63 does not recite the language "60% identical" or "having at least 60% homology." The degree of homology required is precisely that which the Examiner found lacking: enough homology to ensure that the nucleic acid sequence will retain the characteristics of a TfR2. The Examiner observed that a mere single amino acid change can destroy the function of a protein, and found claims 1 and 8 "overly broad" because they could encompass proteins so changed even though they did not "retain the characteristics of a TfR2." The limitations Applicant added to claim 63 avoids this result.

The Applicant respectfully submits that new claims 43-71 fully comport with the requirements of 35 U.S.C. § 112, first paragraph. The Applicant therefore respectfully requests that the Examiner withdraw the objection under this section.

The Examiner objected to claims 1 and 24-30 under 35 U.S.C. § 112, second paragraph as being indefinite, stating that "the phrase 'at least' . . . include[s] elements not actually disclosed (those encompassed by 'at least'), thereby rendering the scope of the claims unascertainable." The Applicant has deleted claims 1 and 24-30. New claims 43-71 do not recite the phrase "at least." The Applicant therefore respectfully requests that the Examiner withdraw the objection under 35 U.S.C. § 112, second paragraph.

The Examiner objected to claim 11 under 35 U.S.C. § 112, second paragraph, stating that the recitation of the term "sufficiently" in claim 11 renders the claim

indefinite. The Applicant has deleted claim 11. New claims 43-71 do not recite the term "sufficiently." The Applicant therefore respectfully requests that the Examiner withdraw the objection under 35 U.S.C. § 112, second paragraph.

The Examiner further objected to claim 11 under 35 U.S.C. § 102(b) as being anticipated by Hiller et al. Hiller et al. discuss the generation of 319,311 express sequence tags ("ESTs") recovered from random cDNA clones. The Examiner has cited to a sequence of mRNA ("Sequence Comparison A"), apparently identified by Hiller et al., which the Examiner states "would hybridize to the mRNA of claim 9, and inhibit translation." The Applicant has deleted claim 11 and replaced it with new claims 59 and 71, directed to an "antisense oligonucleotide complementary to the mRNA of" claims 58 and 70, respectively. The sequence of Hiller et al., in contrast, is not complementary to the mRNA of claims 58 and 70 as claims 59 and 71 require. The Applicant respectfully submits, therefore, that Hiller et al. do not teach, disclose, or suggest the antisense oligonucleotide of claims 59 and 71. The Applicant respectfully requests that the Examiner withdraw the objection to claim 11 under 35 U.S.C. § 102(b).

The Examiner objected to claim 5 and two claims that depended indirectly from it, claims 33 and 34, under 35 U.S.C. § 102(b), stating that a Stratagene catalog teaches the use of random 9-mers capable of hybridizing to the nucleic acid sequences of SEQ ID NOS: 2 and 3. The Applicant has deleted claim 5. None of Applicant's new claims recite the limitation "capable of hybridizing" to the nucleic acid sequences SEQ ID NOS: 2 or 3. The Applicant respectfully requests, therefore, that the Examiner withdraw the objection under 35 U.S.C. § 102(b).

Applicant believes that the foregoing amendments place the application in condition for allowance, and respectfully requests early, favorable action on this application.

If for any reason the Examiner finds the application other than in condition for allowance, the Examiner is requested to call either of the undersigned attorneys at the Los Angeles telephone number (213) 488-7100 to discuss the steps necessary for

placing the application in condition for allowance should the Examiner believe that such a telephone conference would advance prosecution of the application.

Respectfully submitted,

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APPENDIX

IN THE CLAIMS:

The Applicant has canceled claims 1-2, 5-9, 11, 19, and 24-42.

The Applicant has added claims 43-71.